

Baseline Biological Conditions Downstream of Proposed NPDES Outfalls at the Buffalo Mountain Surface Mine, Mingo County, WV May 16-18, 2012

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Background

At the request of EPA Region III's Water Protection Division, aquatic biologists from the Environmental Assessment and Innovation Division's Freshwater Biology Team (FBT) conducted bioassessments of sites located downstream of primary NPDES outlets for CONSOL of KY's Buffalo Mountain Surface Mine. This report documents pre-discharge benthic macroinvertebrates, habitat and physicochemical conditions from 11 sites on six streams draining portions of the Miller Creek and Pigeon Creek of Tug Fork watersheds. The main purpose of the study was to obtain a comparative data set for evaluation of sampling results reported by the applicant and required by the permit. Stations were selected by the applicant and WVDEP to conform to WVDEP's guidance on monitoring NPDES outlets below valley fills associated with the mine operation. Members of the FBT were accompanied by WVDEP, CONSOL, and Baker Associates. The sampling occurred between May 16-18, 2012, approximately 1-2 weeks after the applicant had collected data from these stations.

Study Area

The Buffalo Mountain Surface Mine is located near Delbarton in Mingo County, WV. Mining will occur in the Miller Creek (direct drain to Tug Fork) and Pigeon Creek of Tug Fork watersheds. Mountaintop mining and valley fill spoil disposal is the most common form of coal mining in the Central Appalachians (ecoregion 69d after Woods et al. 1996). The proposed mining will impact roughly 2300 acres with 159 NPDES outlets and 12 valley fills. While most of the outlets are on-bench precipitation-driven outfalls, the outlets draining each valleyfill are relatively permanent waters (RPWs) or occur in perennial flowing streams. EPA's 11 sample locations correspond directly with those outlined in CONSOL's Aquatic Ecosystem Protection Plan (AEPP). The 12th site was eliminated after USACE determined the location of the outfall was not a RPW. The stations are listed in Table 1 and shown in Figures 1 through 4. Station photographs are shown in Appendix A. Sample locations were situated below each valleyfill outfall in reaches of relatively dense riparian forest with 75-100% canopy cover. Based on WVDEP mine permit GIS layers, the proposed cumulative proportion of the watershed disturbed (mining, fills, and treatment ponds) will be substantial (Table 2, ranging from 41 to 86%); primary NPDES outlets will drain 1-2 valley fills.

Table 1. General station and stream identifiers for biological sampling sites.

Station ID	Outfall	Stream Name	Latitude	Longitude	Catchment Area (ac)
BASdPRC094	094	Pigeonroost Creek	37.7174	-82.2084	215
BASdUPC034	034	UNT/Pigeon Creek	37.7372	-82.2062	115
BASdRB087	087	Ruth Trace Branch	37.7653	-82.2473	290
BASdLHC054	054	Left Fork Hell Creek	37.7226	-82.2219	140
BASdLHC083	083	Left Fork Hell Creek	37.7186	-82.2201	380
BASd1RHC062	062	UNT/Right Fork Hell Creek	37.7360	-82.2335	158
BASdRHC051	051	Right Fork Hell Creek	37.7305	-82.2317	108
BASdRHC052	052	Right Fork Hell Creek	37.7292	-82.2301	240
BASdLCB074	074	Left Fork Conley Branch	37.7514	-82.2316	154
BASdMC061	061	Miller Creek	37.7392	-82.2455	1025
BASdRCB098	098	Right Fork Conley Branch	37.7492	-82.2407	294

Table 2. Proposed land use estimates (% mining, % fill) associated with NPDES outfalls listed in Table 1.

Station ID	Sample ID	Stream Name	Proposed Mining (%)	Proposed Fill (%)	# of fills
BASdPRC094	5161201	Pigeonroost Cr.	86	26	1
BASdUPC034	5161202	UNT/Pigeon Cr.	57	23	1
BASdRB087	5161203	Ruth Trace Br.	79	34	1
BASdLHC054	5171201	LF Hell Cr.	79	19	1
BASdLHC083	5171202	LF Hell Cr.	82	14	1
BASd1RHC062	5171203	UNT/RF Hell Cr.	76	35	1
BASdRHC051	5171204	RF Hell Cr.	70	13	1
BASdRHC052	5171205	RF Hell Cr.	69	15	1
BASdLCB074	5171206	LF Conley Br.	52	23	1
BASdMC061	5181201	Miller Cr.	41	6	1
BASdRCB098	5181203	RF Conley Br.	52	18	2

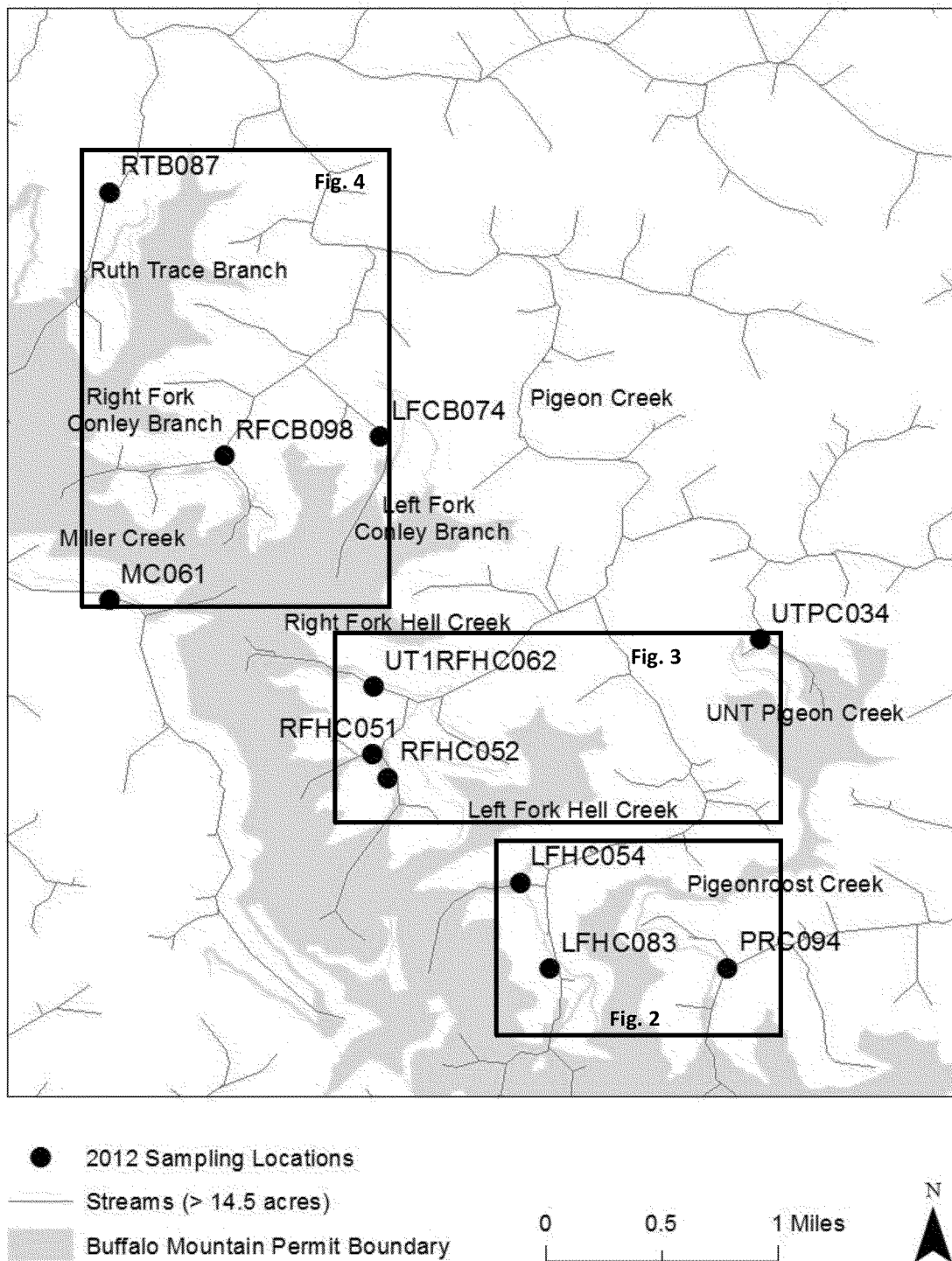


Figure 1. Overview map of study area with mine permit boundaries and sample locations (from AEPP). Rectangles refer to point of reference for specific maps of closeup views (see Figs. 2-4 below).

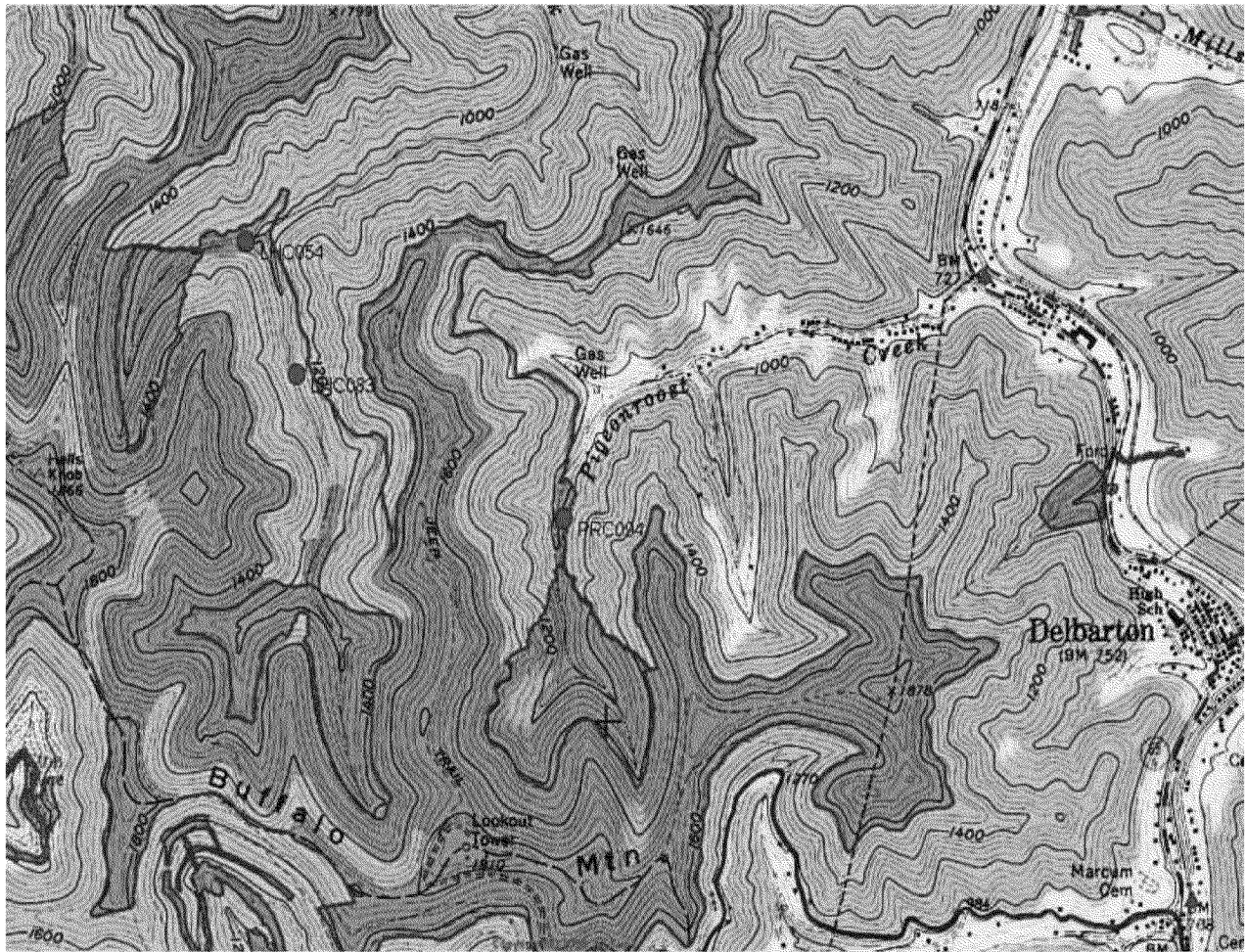


Figure 2. Close-up view of terrain for stations PRC094, LFHC083, and LFHC054. Shaded areas indicate proposed surface disturbance. Refer to Table 1 for full station and stream names.

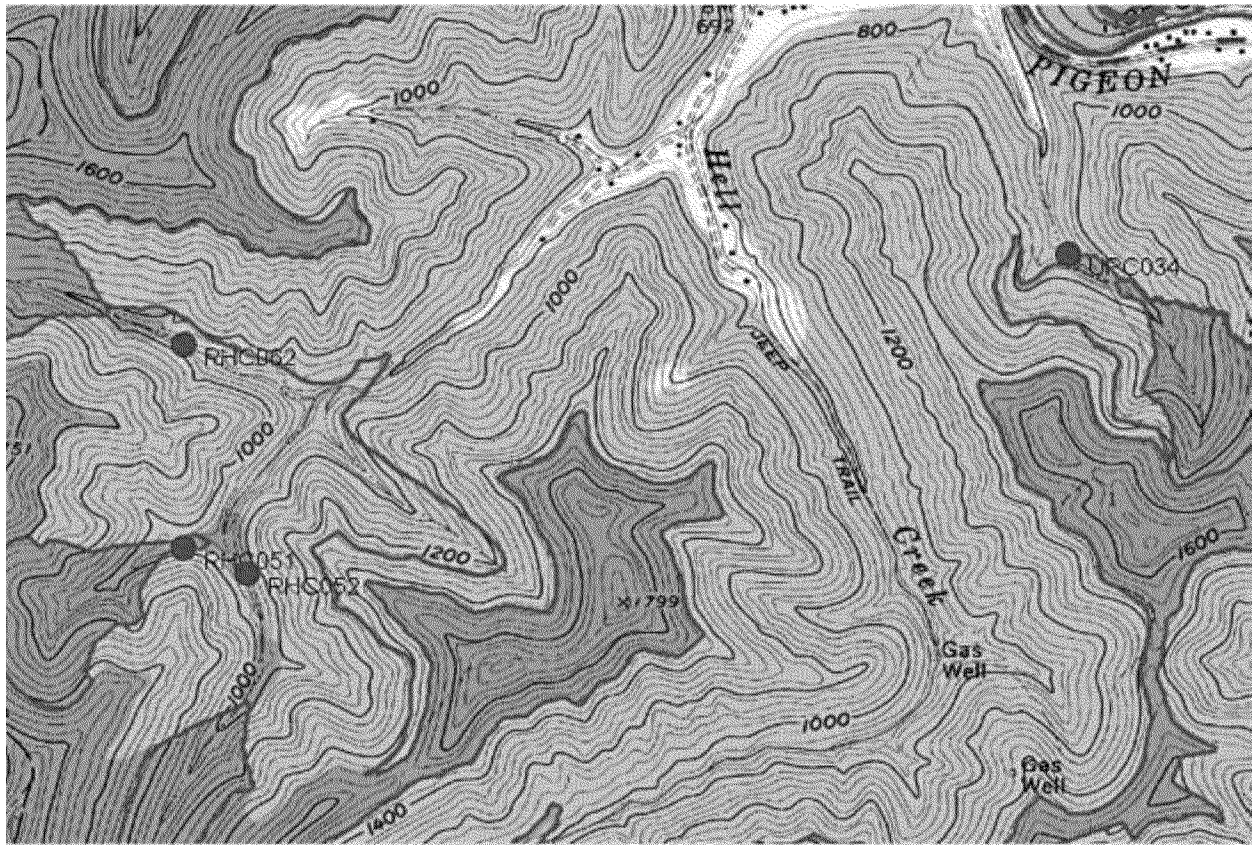


Figure 3. Close-up view of terrain for stations RFHC062, and RFHC051, RFHC052, and UPC034. Shaded areas indicate proposed surface disturbance. Refer to Table 1 for full station and stream names.

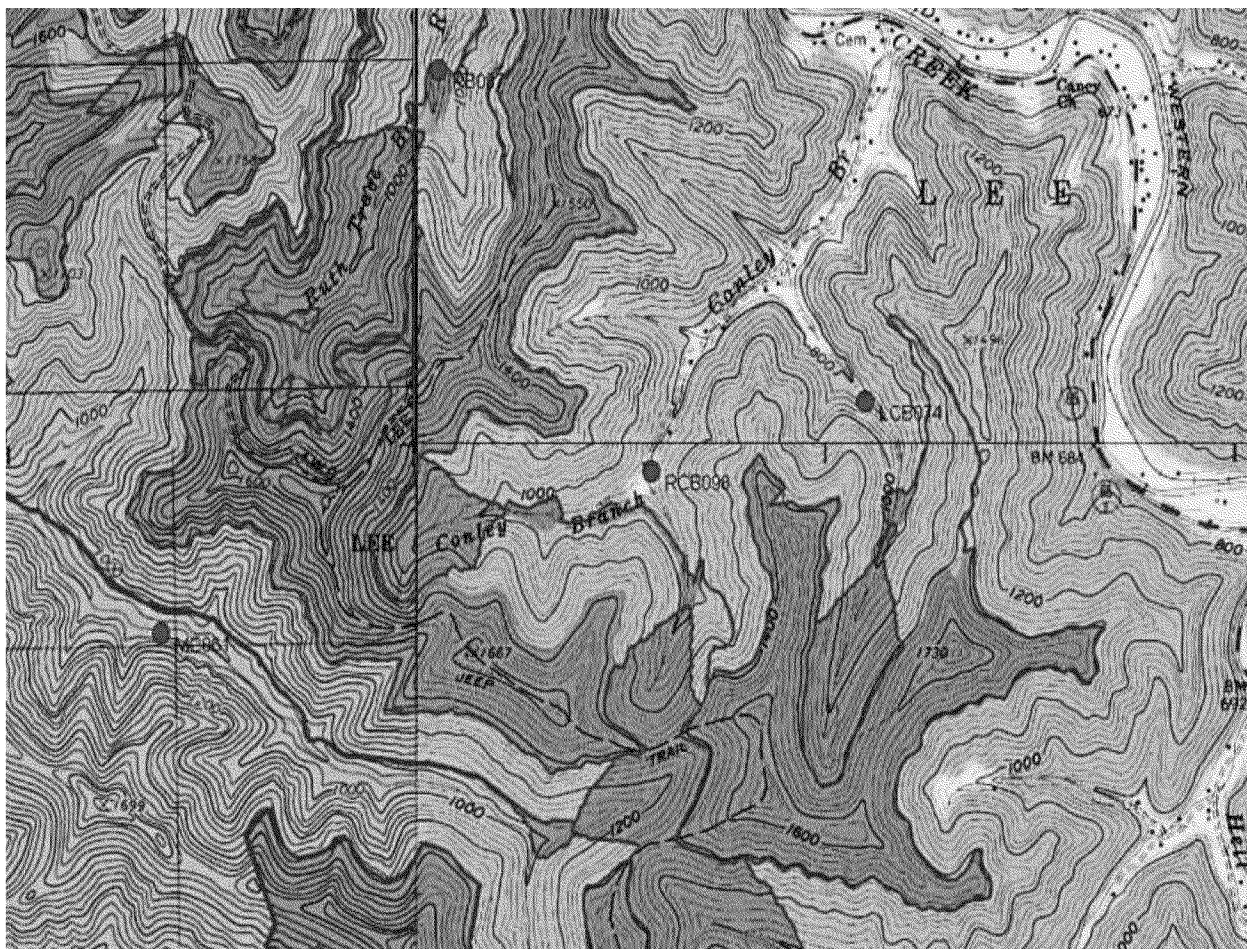


Figure 4. Close-up view of terrain for stations MC061, and RCB98, LCB074, and RB087. Shaded areas indicate proposed surface disturbance. Refer to Table 1 for full station and stream names.

Methods

Data Collection

Benthic macroinvertebrates were sampled in accordance with WVDEP Standard Operations Procedures (WVDEP 2011). Briefly, four 0.25 m² kicknet samples were taken from cobble-gravel substrates in riffles with a 0.5 m rectangular net (595 µm mesh). All four 0.25 m² samples were composited to yield a 1 m² collection. In addition to following the WVDEP protocol, an effort was made to sample similar microhabitat conditions at all sites to reduce variability among and between sites. Samples were preserved in 95% ethyl alcohol. For quality control, one duplicate sample (four 0.25 m² kicknet composite) was collected at Miller Creek (MC061) and processed separately to estimate method and index variability.

Habitat features were scored using the EPA Rapid Bioassessment Protocol (RBP) Habitat Assessment procedure following Barbour et al. (1999). This procedure qualitatively evaluates important habitat components such as epifaunal substrate quantity and quality, embeddedness, velocity/depth regimes, sediment deposition, channel flow status, channel alteration, stream bank stability, bank vegetation protection, and riparian zone width. Individual metrics are scored 0-20; the total RBP habitat score is the sum of all metric scores (200 point maximum). Notes on observations of nonpoint source impacts were also recorded on field data sheets. Within individual benthic samples, substrate types (percentage cover) were estimated within each 0.25 m² kicknet quadrat. We also recorded specific conductance, pH, dissolved oxygen, and stream temperature with a portable meter (Hydrolab Surveyor 4a, Hach Company, Loveland, CO). The Hydrolab meter was calibrated with appropriate standards each morning prior to sampling.

Laboratory Procedures

Samples were rinsed in a USGS #30 sieve before being spread out into a 30 x 20 cm 32-grid enamel sorting pan. A 200 (±20%) organism random subsample was obtained from the gridded tray and organisms were placed in labeled vials containing 70% ethyl alcohol. Identifications were made at the genus level, except for some non-insects (e.g., Turbellaria, annelid and nematode worms) using the most up-to-date taxonomic keys. For quality assurance and control, the FBT routinely performs 10% checks of all samples. For this project one sample was second picked by a taxonomist and one sample was re-identified by a second taxonomist. Percent Difference in Enumeration (PDE), Percent Taxonomic Disagreement (PTD), and Percent Sorting Efficiency (PSE) were calculated for these samples (after Stribling et al. 2003). All samples are archived in the FBT laboratory.

Data Analysis

All raw data (biological, chemical, physical) were entered into the FBT's Microsoft Access database (modeled after WVDEP's WABase). Data proofing was completed on 100% of all entries. Ambiguous taxa (early instar or damaged specimens not identified to target taxonomic level) were counted and recorded in the database but were excluded from index calculations to avoid double counting taxa in richness measures. Four separate biological indices (1 family-level multi-metric index (WVSCI), 1 genus-level index (GLIMPSS), and two genus-level predictive models) were calculated in order to quantify baseline biological conditions. Multi-metric indices are composed of several different metrics which are intended to reflect different ecological attributes of the macroinvertebrate sample (e.g., richness, composition and tolerance) (Barbour et al. 1999). Observed/Expected (O/E) multivariate predictive models are used by some researchers in lieu of multi-metric indices (e.g., Hawkins et al. 2000). Thus, we calculated the family-level West Virginia Stream Condition Index (WVSCI) (Gerritsen 2000), the Genus Level Index of Most Probable Stream Status (GLIMPSS) (Pond et al. 2012), an Appalachian O/E predictive model (Pond and North, in review) and a complimentary index of community similarity (BC index, Pond and North in review). All four of these models were calibrated from state reference site data using specific procedures to ensure that the component metrics making up the indices (WVSCI, GLIMPSS,) or the predictive models (Observed/Expected taxa, BC index) could reliably assess biological conditions

relative to state reference conditions. These types of procedures have been published in the peer-reviewed literature and are widely accepted by state and federal agencies in the U.S. (Barbour et al. 1999).

The family level WVSCI has historically been used by the state of West Virginia to determine aquatic life use support. The genus level GLIMPSS represents a “next generation” multi-metric index for West Virginia streams, but has not yet been fully adopted by the state WVDEP. The genus level GLIMPSS offers several enhancements over the family level WVSCI. The finer taxonomic level used in GLIMPSS more accurately depicts the aquatic life present in streams and the true tolerances of the organisms, and provides more range in metric values. The GLIMPSS uses metrics which more accurately reflect the majority of the organisms making up the aquatic life use in these streams. The GLIMPSS regional reference condition was also refined with stratification of sampling season and geographic region, whereas the family-level WVSCI applies only one reference condition statewide.

The multivariate predictive model compared the observed (O) to the expected (E) taxa predicted to occur at each site. The number of expected taxa (E) is the sum of the probabilities of organism capture (P_c) given the environmental setting of the sampling site. P_c 's ≥ 0.5 were used because O/E is more precise and also more sensitive using common taxa. Observed taxa include only those that are actually predicted to occur at the site. The $O/E_{0.5}$ model uses Level IV subcoregion, latitude, and Julian day of sampling as predictor variables (Pond and North, in review). The O/E and BC models were developed using combined WV and KY data for ecoregion 69. The model flags sites that are outside of the model's experience (based on Chi-square test of predictors from model centroids) in order to avoid false predictions.

We chose to compare assessment results with multiple indices because these assessment “tools” are calibrated for use in the Central Appalachian ecoregion and are currently being used by state and federal agencies to assess stream impacts. Multimetric indices can theoretically range from 0-100, but tend to range from about 20 to 90, with higher scores representing better biological conditions and lower scores indicating impairment of the aquatic life use. Predictive models such as $O/E_{0.5}$ generally range from 0 to 1.5, with a score of 1.0 indicating a perfect match of observed to expected taxa. Values > 1 can occur because expected taxa have probability of capture values < 1 , while observed taxa are assigned an observed value of 1. The BC index ranges from 0 to 1 with lower scores indicating better conditions. The BC index offers a refinement over the O/E model in that it tries to correct for actual loss of taxa. Aquatic life use impairment thresholds are based on regional reference conditions developed by WV DEP (Gerritsen et al. 2000, Pond et al. 2012) and are calculated using the 5th percentile of independent reference site index scores. Percent of threshold values were calculated to normalize index scores for comparative purposes. For these data, we used the following impairment thresholds:

GLIMPSS= 53; where % of threshold = site score/53*100

WVSCI =68; where % of threshold = site score/68*100

$O/E_{0.5}$ =0.77; where % of threshold = site score/0.77*100

BC= 0.37; where % of threshold = 0.37/site score*100

Finally, a two-way cluster analysis (sites and taxa) was performed for illustrative purposes. This technique used the flexible beta clustering procedure (PC-ORD v. 6, Gleneden, OR) with Bray-Curtis similarity (distance) matrix. We excluded less common taxa across sites (frequency <25%) to focus on most prevalent taxa (48 taxa); results are displayed as a two-way dendrogram.

Results

Habitat and Physicochemical Data

At the time of sampling, seasonal water levels were normal and all streams were running relatively clear. No unusual odors or surface oils were observed. Table 3 summarizes physicochemical observations (pH, specific conductance, temperature, and dissolved oxygen). All sites were circumneutral to slightly acidic and relatively dilute. Conductivity ranged from 32 to 152 $\mu\text{S}/\text{cm}$ and pH ranged from 6.02 to 7.25. Streams with conductivities >125 $\mu\text{S}/\text{cm}$ might suggest some abandoned deep mine discharges but with minimal influence on water quality at those stations. Dissolved oxygen and stream temperature were all within normal limits for streams sampled this time of year.

Table 3. In situ physicochemical measurements recorded May 16-18, 2012.

Station ID	Sample ID	Stream Name	pH	Sp Cond	Temp (oC)	DO (mg/L)
BASdPRC094	5161201	Pigeonroost Cr.	6.67	46.10	16.24	9.56
BASdUPC034	5161202	UNT/Pigeon Cr.	6.47	45.10	15.26	9.59
BASdRB087	5161203	Ruth Trace Br.	6.33	32.20	16.35	9.38
BASdLHC054	5171201	LF Hell Cr.	6.31	78.90	14.28	9.81
BASdLHC083	5171202	LF Hell Cr.	6.02	50.10	14.30	9.68
BASd1RHC062	5171203	UNT/RF Hell Cr.	6.05	43.20	15.66	9.51
BASdRHC051	5171204	RF Hell Cr.	6.99	126.70	16.16	9.56
BASdRHC052	5171205	RF Hell Cr.	7.10	152.20	16.21	9.54
BASdLCB074	5171206	LF Conley Br.	6.27	47.50	15.87	9.38
BASdMC061	5181202	Miller Cr.	7.25	146.80	13.34	10.04
BASdRCB098	5181203	RF Conley Br.	6.63	43.20	14.53	9.81

Table 4 summarizes RBP Habitat scores for the 11 monitoring stations. Habitat scores were in the sub-optimal to optimal range (average = 141.4, range=127 to 160). Most of these sites could qualify as reference quality by WVDEP based on habitat and water quality. Stations with lower habitat scores typically had long stretches of bedrock in the 100 meter assessed reach. In most cases, the bedrock was intermingled with large woody debris dams, boulders, large cobble and other structures, particularly near the bank margins. In some streams, long stretches of bedrock were representative of the entire stream, in other streams this was not the case. Long stretches of bedrock typically led to low parameter scores for epifaunal substrate and frequency of riffles, since quality of riffle habitat is also considered in scoring this parameter. Some sites also had excessive sedimentation (i.e., scores of 6 and 7). We do not believe some of the applicant's sites are fully representative of the potential habitat conditions in these streams. As the sites were selected to conform to the NPDES outlets, this often resulted in sampling

areas with compromised habitat (e.g., high proportion of bedrock, bank erosion, or an adjacent residence in one instance).

Table 5 shows substrate composition (visual/textural estimates) among composited riffle kicknet samples. Delineated benthic sample habitats were comprised primarily by cobble and gravel (~90% combined). Coarse gravel made up the majority of the % gravel estimates. Full pebble count data (and substrate distributions) for these sites are reported by CONSOL in their AEPP. At all sites, benthic algae and aquatic mosses were present but low in abundance; filamentous green algae (e.g., *Cladophora*) or vascular aquatic plants were absent. However, on fast-water bedrock substrates, the red algae, *Lemanea*, was observed at most sites. This perennial red algal genus is commonly found in clean watersheds and does not typically reach nuisance levels.

Table 4. RBP Habitat scores recorded May 16-18, 2012. Note: low epifaunal and riffle frequency scores at some sites due to extensive bedrock in reach.

Station ID	Stream Name	Epifaunal Substrate	Embedded-ness	Velocity/Depth	Channel Alteration	Sediment Deposition	Riffle Frequency	Channel Flow Status	Total Bank Stability	Total Bank Vegetative Protection	Total Rip Veg Zone	Total RBP Score
BASdPRC094	Pigeonroost Cr.	13	17	10	19	14	15	17	18	17	20	160
BASdUPC034	UNT/Pigeon Cr.	6	17	10	19	11	5	11	18	16	18	131
BASdRB087	Ruth Trace Br.	13	15	10	15	7	15	15	14	15	18	137
BASdLHC054	LF Hell Cr.	15	17	10	15	9	18	11	13	14	17	139
BASdLHC083	LF Hell Cr.	18	16	10	19	10	16	10	18	18	19	154
BASd1RHC062	UNT/RF Hell Cr.	11	15	10	18	6	11	9	16	16	17	129
BASdRHC051	RF Hell Cr.	11	16	10	12	7	15	10	14	17	15	127
BASdRHC052	RF Hell Cr.	15	16	10	18	13	16	15	14	16	20	153
BASdLCB074	LF Conley Br.	17	14	10	19	10	18	15	15	18	20	156
BASdMC061	Miller Cr.	13	14	10	16	10	15	15	14	17	18	142
BASdRCB098	RF Conley Br.	15	12	10	14	10	17	10	16	13	10	127

Table 5. Substrate composition within benthic kick samples collected May 16-18, 2012.

Station ID	Stream Name	% Bedrock	% Boulder	% Cobble	% Gravel	% Sand	% Silt	% Clay		% Coarse Gravel	% Fine Gravel
BASdPRC094	Pigeonroost Cr.	0	0	40	55	5	0	0		40	15
BASdUPC034	UNT/Pigeon Cr.	0	0	30	70	0	0	0		50	20
BASdRB087	Ruth Trace Br.	0	5	50	35	10	0	0		25	10
BASdLHC054	LF Hell Cr.	0	0	50	45	5	0	0		40	5
BASdLHC083	LF Hell Cr.	0	5	40	50	5	0	0		40	10
BASd1RHC062	UNT/RF Hell Cr.	0	5	35	55	5	0	0		40	15
BASdRHC051	RF Hell Cr.	0	0	60	35	5	0	0		30	5
BASdRHC052	RF Hell Cr.	0	0	60	35	5	0	0		30	5
BASdLCB074	LF Conley Br.	0	0	65	30	5	0	0		25	10
BASdMC061	Miller Cr.	0	0	65	30	5	0	0		20	10
BASdRCB098	RF Conley Br.	0	0	60	30	10	0	0		20	10
	Mean	0.0	1.4	50.5	42.7	5.5	0.0	0.0		32.7	10.5
	SD	0.0	2.3	12.5	13.3	2.7	0.0	0.0		9.8	4.7

Biological Data

Taxa lists and counts for all samples are reported in Appendix B. Table 6 summarizes GLIMPSS, WVSCI, O/E_{0.5}, and BC indicators across all stations. None of the sites were flagged as outliers for the predictive model (O/E). The baseline conditions indicate very high quality biological communities; the 11 stations averaged 145% of the respective impairment threshold for GLIMPSS, 133% for WVSCI, 124% for O/E_{0.5}, and 113% for BC. Standard deviations of these bioindicators were low indicating that the 11 sites were all relatively similar to each other. When compared to independent bioassessment data from WVDEP (n=225 in ecoregion 69d for spring season), on average, our baseline Buffalo Mountain GLIMPSS scores rank at the 90th percentile (range= 85th to 95th percentile) while average WVSCI scores rank at the 85th percentile (range= 75th to 90th percentile). Estimated densities (based on number of random grids picked to achieve target subsample) averaged 1292 individuals/m² (range= 544 to 1680/m²); Miller Creek samples (includes duplicate) had the lowest densities among stations.

Table 7 lists example metrics values (including GLIMPSS MT Sp) for each station. Taxonomically, these 11 sites were diverse, having 30 to 44 total taxa in riffle kicknet samples (200 (±20%) subsamples). Richness for Ephemeroptera, Plecoptera, and Trichoptera (EPT) genera averaged 18 taxa (range= 16 to 21 genera) across all samples. Mayflies (E) ranged from 6 to 11 taxa, stoneflies (P) ranged from 4 to 9 taxa, and caddisflies (T) ranged from 3 to 6 taxa. The number of all intolerant taxa (tolerance value<4) averaged 16 taxa and ranged from 13 to 23; scraper richness averaged 7 taxa (range= 4 to 9). Mayflies made up a large proportion of the community at each site, ranging in relative abundance from 21 to 55% (average=31.9%). Clinger richness (a potential measure of sedimentation effects) was high and averaged 16.2 (range=13 to 19 taxa).

Figure 5 displays a two-way dendrogram of most prevalent taxa across sites. The site cluster analysis indicated that assemblage-wise, Miller Creek (and duplicate) was relatively distinct from other sites; it was the largest stream we sampled and had relatively higher pH and conductivity compared to other sites. Nine taxa were collected at >90% of sites. These ubiquitous taxa are not necessarily the most sensitive to disturbance, but could be used to track biological changes after mining commences. However, each site-specific community (draining each NPDES outlet) should be evaluated individually in future assessments. Cluster analysis could be used as a supplementary tool in future assessments to help further determine if any departure from baseline has occurred, as it is an efficient graphical technique to visualize changes in the entire assemblage.

Fourteen genera found in our baseline samples are predicted to be extirpated if specific conductance increases. At 500 µS/cm (the action trigger under the permit), species sensitivity distribution modeling (SSD) published by US EPA (2011) predicts that *Agapetus*, *Drunella*, *Eccopectura*, *Epeorus*, *Ephemerella*, *Eurylophella*, *Haploperla*, *Isoperla*, *Lepidostoma*, *Leucrocota*, *Neophylax*, *Paraleptophlebia*, *Pycnopsyche*, and *Remenus* could be extirpated from sites in the project area. On a project-wide basis, this could account for 17% taxa loss (14 of 82 genera with modeled extirpation concentrations) if conductivity exceeds 500 µS/cm. Since our samples were collected in mid-May, other conductivity-sensitive taxa are likely to occur at these sites (e.g., *Cinygmula*, *Alloperla*, *Demicryptochironomus*, *Diploperla*, *Paracapnia*)

but were absent possibly due to life-history phenology. Three of these other taxa were collected by CONSOL, 2 weeks prior to our sampling as part of their AEPP sampling. By way of example, Figure 6 depicts site-specific SSDs for two sites: UNT Pigeon Creek and Right Fork Hell Creek where on average, 22% and 14% of observed genera are predicted to be extirpated if conductivity exceeds 500 $\mu\text{S}/\text{cm}$, respectively.

Summary of QA/QC

Laboratory QA/QC values were excellent and passed all processing and identification criteria (PDE=2.1%, PTD=8.8%, PSE=0.0%). By comparison, precision criteria for the EPA's National Rivers and Stream Assessment (NRSA) are PDE=10%, PTD= 15%, and PSE=10%. EAID's Freshwater Biology Laboratory long-term average QA/QC statistics (>10 yrs) are 2.8% PDE, 8.7% PTD, and 3.5% PSE. For sampling precision, the duplicate sample was collected at Miller Creek (MC061). The two Miller Creek samples scored nearly identical for GLIMPSS (73.6 and 72.9) and were identical for WVSCI (89.9 for both). These results indicate that sampling, processing, and laboratory methodology used in this study had high levels of precision.

Table 6. Biological indicator scores and estimated macroinvertebrate density for samples taken May 16-18, 2012. Percent of thresholds (5th percentile of independent WVDEP reference sites) calculated to normalize index scores for comparative purposes. Density estimates based on proportion of grids picked to reach target subsample with the 1 m² sample.

Station ID	Sample ID	Stream Name	GLIMPSS	GLIMPSS % of threshold	WVSCI	WVSCI % of threshold	O/E _{0.5}	O/E % of threshold	BC	BC % of threshold	Density no/m ²
BASdPRC094	5161201	Pigeonroost Cr.	79.6	150.3	91.3	134.2	0.92	119.1	0.33	113.1	1560.0
BASdUPC034	5161202	UNT/Pigeon Cr.	83.0	156.6	89.3	131.3	0.96	124.5	0.32	114.9	1235.2
BASdRB087	5161203	Ruth Trace Br.	76.9	145.2	93.4	137.3	1.00	129.3	0.33	111.4	1464.0
BASdLHC054	5171201	LF Hell Cr.	77.2	145.7	87.9	129.2	0.96	124.5	0.34	108.3	1552.0
BASdLHC083	5171202	LF Hell Cr.	73.7	139.1	90.1	132.5	0.88	114.1	0.34	108.2	1672.0
BASd1RHC062	5171203	UNT/RF Hell Cr.	77.3	145.8	92.7	136.3	0.96	124.3	0.31	118.3	1680.0
BASdRHC051	5171204	RF Hell Cr.	85.0	160.4	93.0	136.8	1.20	155.5	0.26	142.7	1280.0
BASdRHC052	5171205	RF Hell Cr.	77.8	146.8	92.7	136.3	0.96	124.4	0.34	110.0	1576.0
BASdLCB074	5171206	LF Conley Br.	73.8	139.2	90.8	133.6	0.92	119.3	0.33	111.6	1002.7
BASdMC061	5181201	Miller Cr.	73.6	139.0	89.9	132.2	0.77	100.0	0.38	97.4	923.4
BASdMC061	5181202	Miller Cr. (duplicate)	72.9	137.5	89.9	132.1	0.99	129.2	0.32	117.2	544.0
BASdRCB098	5181203	RF Conley Br.	75.9	143.2	85.4	125.5	0.99	129.1	0.34	109.9	1013.3
		Mean	77.2	145.7	90.5	133.1	0.96	124.4	0.33	113.6	1291.9
		SD	3.79	7.16	2.35	3.46	0.10	12.75	0.03	10.61	357.35

Table 7. GLIMPSS metric values (Mountain Spring stratum) for all samples collected May 16-18, 2012.

Station ID	Stream Name	Sample ID	Total Individuals (subsample)	# Total Taxa	# Intolerant Taxa <4	# EPT Taxa	# Ephemeroptera Taxa	# Plecoptera Taxa	# Trichoptera Taxa	# Clinger Taxa	% Ephemeroptera	HBI (Generic)	% 5 Dominant Taxa	% Orthocladinae	# Scraper Taxa	# Shredder Taxa
BASdPRC094	Pigeonroost Cr.	5161201	195	39	16	19	8	7	4	17	30.8	3.56	52.8	8.2	7	6
BASdUPC034	UNT/Pigeon Cr.	5161202	193	44	23	20	9	7	4	17	30.1	3.47	50.8	13.5	9	8
BASdRB087	Ruth Trace Br.	5161203	183	36	13	17	9	5	3	17	37.2	3.21	62.3	3.8	8	4
BASdLHC054	LF Hell Cr.	5171201	194	37	15	18	8	4	6	18	27.3	3.33	65.0	13.9	7	4
BASdLHC083	LF Hell Cr.	5171202	209	32	13	17	9	5	3	14	22.0	2.70	65.6	7.2	7	5
BASd1RHC062	UNT/RF Hell Cr.	5171203	210	37	15	16	6	5	5	15	22.9	3.26	57.1	4.3	8	6
BASdRHC051	RF Hell Cr.	5171204	200	38	15	21	9	6	6	19	30.5	3.15	54.0	5.5	7	5
BASdRHC052	RF Hell Cr.	5171205	197	35	17	19	7	9	3	17	28.4	3.57	54.3	5.6	6	6
BASdLCB074	LF Conley Br.	5171206	188	42	20	17	6	7	4	14	21.8	3.37	45.7	8.5	4	5
BASdMC061	Miller Cr.	5181201	202	36	16	17	6	7	4	15	39.1	3.79	55.9	10.9	6	7
BASdMC061	Miller Cr. (duplicate)	5181202	187	34	13	19	11	5	3	13	37.4	3.64	54.6	10.2	7	6
BASdRCB098	RF Conley Br.	5181203	190	30	16	17	7	6	4	18	55.3	3.77	75.3	2.1	9	1
	Mean		196	36.7	16.0	18.1	7.9	6.1	4.1	16.2	31.9	3.4	57.8	7.8	7.1	5.3
	SD		8.4	3.9	3.0	1.5	1.6	1.4	1.1	1.9	9.4	0.3	8.0	3.8	1.4	1.8

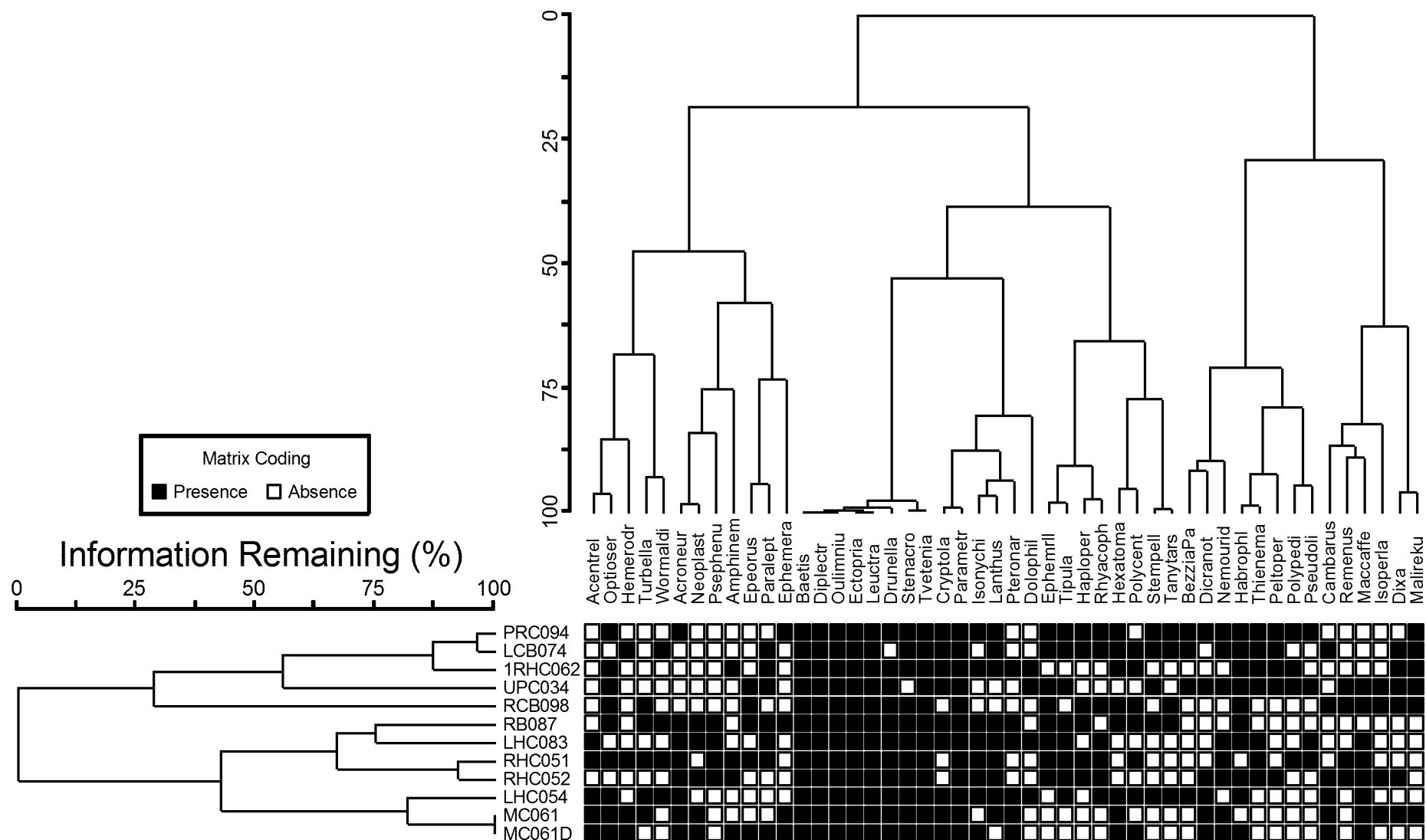


Figure 5. Two-way cluster dendrogram of sites and taxa based on 200-subsample using flexible beta procedure with Bray-Curtis similarity coefficients. Only taxa collected at >25% of all sites plotted for brevity (48 taxa).

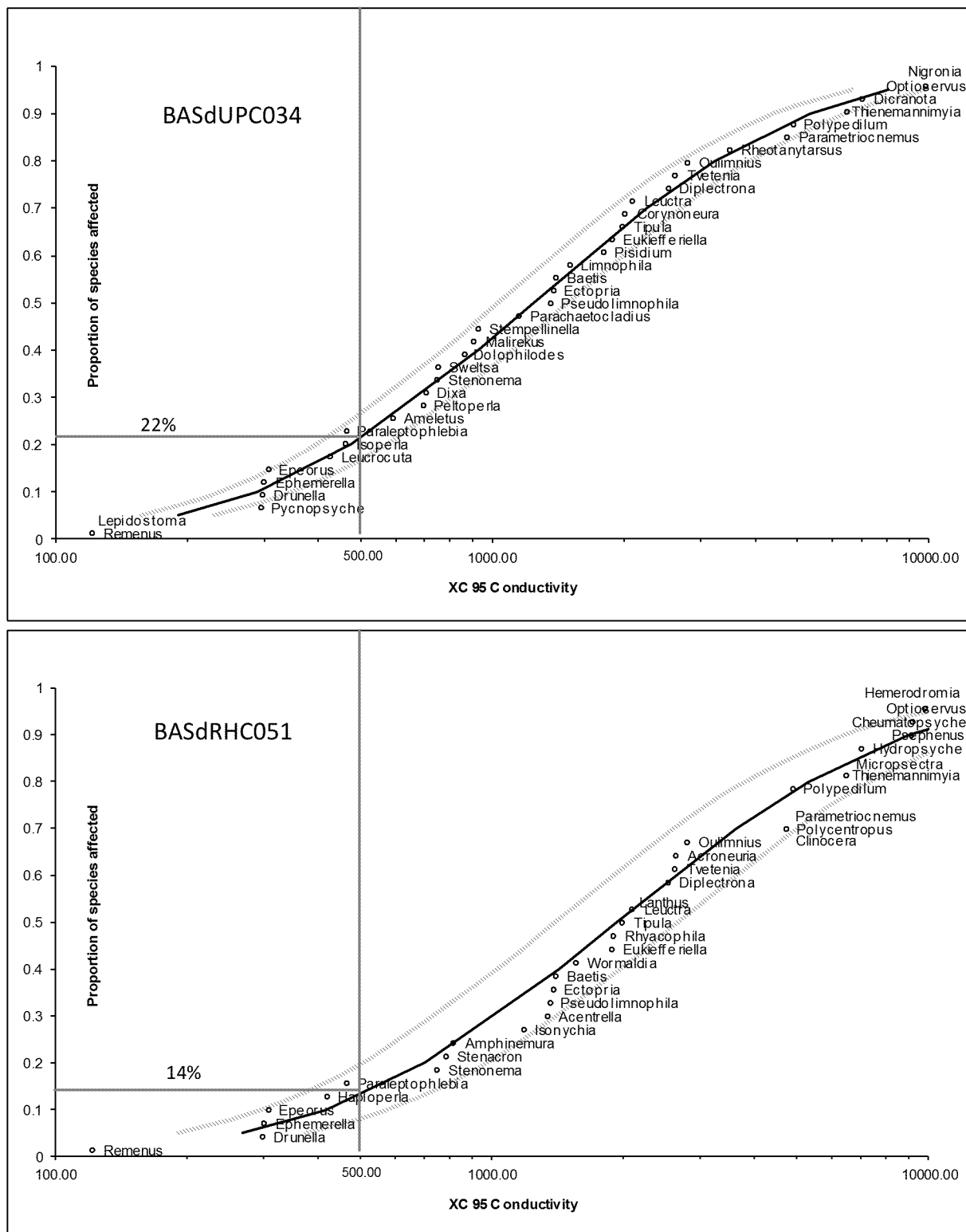


Figure 6. Example site-specific SSDs for EPA samples from UNT Pigeon Creek (BASdUPC034; top) and Right Fork Hell Creek (BASdRHC051; bottom) showing proportion of species (genera) predicted to be lost at 500 $\mu\text{S}/\text{cm}$.

Conclusion and Recommendations

Baseline conditions downstream of the proposed primary NPDES outlets exhibit excellent biological and water quality comparable to WVDEP's least-disturbed reference condition network. Despite some habitat limitations at some sites (e.g., a high proportion of bedrock and moderate, localized sedimentation), macroinvertebrate assemblages were diverse, and mostly comprised of sensitive taxa at the 11 sites. All bioassessment indicators used in this report should be considered for during-mining and post-mining assessments in a weight-of-evidence approach as they provide different information on biological condition to the assessment. We believe this one time sample event is representative of spring-season baseline biological conditions. For this permit, future monitoring and assessment should take place on or around this anniversary date to detect changes in biological conditions.

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Appendix A. Site photographs taken May 16-18, 2012.



PRC094-Pigeonroost Creek



UPC034-UNT Pigeon Creek



RB087-Ruth Trace Branch



LHC054-Left Fork Hell Creek



LHC083-Left Fork Hell Creek



RHC062-UNT/Right Fork Hell Creek



RHC051-Right Fork Hell Creek



RHC052-Right Fork Hell Creek



LCB074-Left Fork Conley Branch



MC061-Miller Creek



RCB098-Right Fork Conley Branch

Appendix B. List of macroinvertebrate genera and counts for Buffalo Mountain baseline samples (May 16-18, 2012).

			Pigeonroost Cr.	UNT/Pigeon Cr.	Ruth Trace Br.	LF Hell Cr.	LF Hell Cr.	RF Hell Cr.	RF Hell Cr.	RF Hell Cr.	LF Conley Br.	Miller Cr.	Miller Cr. (dup)	RF Conley Br.
			PRC094	UPC034	RB087	LHC054	LHC083	1RHC062	RHC051	RHC052	LCB074	MC061	MC061	RCB098
Turbellaria	Turbellaria	Turbellaria			1	1			1			1		1
Veneroida	Pisidiidae	<i>Pisidium</i>		1								1		
Haplotaxida	Enchytraeidae	Enchytraeidae								1				
Haplotaxida	Lumbricidae	Lumbricidae												1
Haplotaxida	Naididae	Naididae		1										
Haplotaxida	Tubificidae	Tubificidae							5	11				1
Lumbriculida	Lumbriculidae	Lumbriculidae		6	1			1						
Ephemeroptera	Ameletidae	<i>Ameletus</i>		1										
Ephemeroptera	Baetidae	<i>Acentrella</i>				6	1		5			12		18
Ephemeroptera	Baetidae	<i>Baetis</i>	18	7	25	31	23	22	30	31	16	35	17	86
Ephemeroptera	Baetidae	<i>Dipheter</i>									3			1
Ephemeroptera	Ephemerellidae	<i>Drunella</i>	3	1	10	6	11	2	7	5		6	4	5
Ephemeroptera	Ephemerellidae	<i>Ephemerella</i>	2	2	3		1		4	1	2			1
Ephemeroptera	Ephemerellidae	<i>Eurylophella</i>	1											
Ephemeroptera	Ephemeridae	<i>Ephemer</i>	1		4							1		1
Ephemeroptera	Heptageniidae	<i>Epeorus</i>		3	2				1					1
Ephemeroptera	Heptageniidae	<i>Leucocuta</i>		3		1								3
Ephemeroptera	Heptageniidae	<i>Maccaffertium</i>		1		2	1		3	3		1		1
Ephemeroptera	Heptageniidae	<i>Stenacron</i>	12		11	4	1	5	9	12	5	24	21	6
Ephemeroptera	Isonychiidae	<i>Isonychia</i>	2		4	2	6	1	1	1				3
Ephemeroptera	Leptophlebiidae	<i>Habrophlebiodes</i>	21	35	4	1	1	16		3	14			1
Ephemeroptera	Leptophlebiidae	<i>Paraleptophlebia</i>		5	5		1	2	1		1			2
Odonata	Aeshnidae	<i>Boyeria</i>									1			
Odonata	Gomphidae	<i>Gomphidae</i>				3				4				
Odonata	Gomphidae	<i>Lanthus</i>	3		10		4	6	4		1	2		
Plecoptera	Chloroperlidae	<i>Haploperla</i>	1		1				2	1	3			2
Plecoptera	Chloroperlidae	<i>Sweltsa</i>	1	1							2			
Plecoptera	Leuctridae	<i>Leuctra</i>	31	24	36	43	60	43	46	31	36	23		29
Plecoptera	Nemouridae	<i>Amphinemura</i>						1	2	5				2
Plecoptera	Nemouridae	Nemouridae	2				1		1	2	2	1		1
Plecoptera	Nemouridae	<i>Soyedina</i>		17										
Plecoptera	Peltoperlidae	<i>Peltoperla</i>	3	2				7		1	1			
Plecoptera	Perlidae	<i>Acronemura</i>	1		1	1	3		5	3		2		5
Plecoptera	Perlidae	<i>Ecoptura</i>				1						1		
Plecoptera	Perlidae	Perlidae					1							
Plecoptera	Perlodidae	<i>Isoperla</i>		1						2		8		1
Plecoptera	Perlodidae	<i>Malirekus</i>	1	7				1			1	1		6
Plecoptera	Perlodidae	Perlodidae			2					8				
Plecoptera	Perlodidae	<i>Remenus</i>		1					1	1				2
Plecoptera	Perlodidae	<i>Yugus</i>									3			1
Plecoptera	Pteronarcyidae	<i>Pteronarcys</i>			3	1	3	1				2		1
Megaloptera	Corydalidae	<i>Nigronia</i>		4		1		1						
Trichoptera	Glossosomatidae	<i>Agapetus</i>						1						
Trichoptera	Glossosomatidae	<i>Glossosoma</i>										1		
Trichoptera	Hydropsychidae	<i>Ceratopsyche</i>	2			1								7
Trichoptera	Hydropsychidae	<i>Cheumatopsyche</i>							2			1		
Trichoptera	Hydropsychidae	<i>Diplectrona</i>	13	3	6	6	12	7	14	18	7	4	5	3
Trichoptera	Hydropsychidae	<i>Hydropsyche</i>							1	1				
Trichoptera	Lepidostomatidae	<i>Lepidostoma</i>		1										
Trichoptera	Limnephilidae	<i>Pycnopsyche</i>		1								1		
Trichoptera	Philopotamidae	<i>Dolophilodes</i>		3		2	7	4						
Trichoptera	Philopotamidae	<i>Wormaldia</i>			1	2			2		1			
Trichoptera	Polycentropodidae	<i>Polycentropus</i>			1	1		2	2		11			1
Trichoptera	Rhyacophillidae	<i>Rhyacophila</i>	1			1	1		1	1	4			1
Trichoptera	Uenoidae	<i>Neophylax</i>	1					7						1
Coleoptera	Dryopidae	<i>Helichus</i>	1		1		5							
Coleoptera	Elmidae	<i>Optioservus</i>	2	1	1	3		1	7			10	5	1
Coleoptera	Elmidae	<i>Oulimnius</i>	6	1	4	8	7	6	9	15	8	16	15	2
Coleoptera	Elmidae	<i>Stenelmis</i>						1			3			2
Coleoptera	Psephenidae	<i>Ectopria</i>	20	7	22	4	10	17	5	10	5	3	10	2
Coleoptera	Psephenidae	<i>Psephenus</i>			3		2		6	2				
Coleoptera	Ptilodactylidae	<i>Anchytarsus</i>												1

Appendix B. Continued.

Order	Family	Genus	5161201	5161202	5161203	5171201	5171202	5171203	5171204	5171205	5171206	5181201	5181202	5181203
			Pigeonroost Cr.	UNT/Pigeon Cr.	Ruth Trace Br.	LF Hell Cr.	LF Hell Cr.	RF Hell Cr.	RF Hell Cr.	RF Hell Cr.	LF Conley Br.	Miller Cr.	Miller Cr. (dup)	RF Conley Br.
			PRC094	UPC034	RB087	LHC054	LHC083	1RHC062	RHC051	RHC052	LCB074	MC061	MC061	RCB098
Diptera	Dixidae	<i>Dixa</i>		2				10		1	3	1		8
Diptera	Empididae	<i>Chellifera/Metach</i>	1			1		1						
Diptera	Empididae	<i>Clinocera</i>							2					
Diptera	Empididae	<i>Hemerodromia</i>							2		2	1	1	
Diptera	Empididae	<i>Neoplasta</i>			1		6			2		3	5	
Diptera	Empididae	<i>Trichoclinocera</i>				1								
Diptera	Ephydriidae	<i>Cirrula</i>						1						
Diptera	Sciaridae	<i>Corynoptera</i>						1						
Diptera	Simuliidae	<i>Simulium</i>			1					2				
Diptera	Tipulidae	<i>Antocha</i>										1		
Diptera	Tipulidae	<i>Cryptolabis</i>	7	1	1	17	20	22			9	9	4	
Diptera	Tipulidae	<i>Dicranota</i>	2	4		2				2		4	2	
Diptera	Tipulidae	<i>Hexatoma</i>	2		2	2		4			7	2	1	1
Diptera	Tipulidae	<i>Limnophila</i>		1							1			1
Diptera	Tipulidae	<i>Molophilus</i>								1				
Diptera	Tipulidae	<i>Ormosia</i>									1			
Diptera	Tipulidae	<i>Pseudolimnophila</i>	5	3			1		1					
Diptera	Tipulidae	<i>Tipula</i>	2	1	1	4	1		2	1	1			
Diptera	Ceratopogonidae	<i>Atrichopogon</i>									1			
Diptera	Ceratopogonidae	<i>Bezzia/Palpomyia</i>	1	2		2					1			
Diptera	Ceratopogonidae	<i>Ceratopogon</i>	1											
Diptera	Chironomidae	<i>Brillia</i>										1		
Diptera	Chironomidae	<i>Chaetocladius</i>	1											
Diptera	Chironomidae	<i>Corynoneura</i>		1			1							
Diptera	Chironomidae	<i>Cricotopus</i>										1		
Diptera	Chironomidae	<i>Epoicocladius</i>			1								1	
Diptera	Chironomidae	<i>Eukiefferiella</i>		2			1		3					
Diptera	Chironomidae	<i>Heleniella</i>									1			
Diptera	Chironomidae	<i>Krenosmittia</i>									2			
Diptera	Chironomidae	<i>Lopescladius</i>									1			
Diptera	Chironomidae	<i>Micropsectra</i>				1			2		1			
Diptera	Chironomidae	<i>Orthocladius</i>					1	1				1		
Diptera	Chironomidae	<i>Parachaetocladiu</i>		1				1			1			
Diptera	Chironomidae	<i>Parametriochnemu</i>	5	7	2	8	11	4	1	3	4	4	1	1
Diptera	Chironomidae	<i>Polypedilum</i>	1	2				1	1					
Diptera	Chironomidae	<i>Psilometriochnemu</i>		2										
Diptera	Chironomidae	<i>Rheosmittia</i>												1
Diptera	Chironomidae	<i>Rheotanytarsus</i>		1										
Diptera	Chironomidae	<i>Stempellinella</i>	1	1	3	2					2			
Diptera	Chironomidae	<i>Stilocladius</i>						1						
Diptera	Chironomidae	<i>Tanypodinae</i>			1			1						
Diptera	Chironomidae	<i>Tanytarsus</i>	2		4	2					5			1
Diptera	Chironomidae	<i>Thienemannimyia</i>	5	9			4	5	2	1	5			
Diptera	Chironomidae	<i>Tvetenia</i>	10	13	4	19	1	2	7	8	7	15	17	2
Decapoda	Cambaridae	<i>Cambarus</i>				1				3	3	2	1	5